

SEQUENCE LISTING

<110> Chen et al.

<120> METHODS AND COMPOSITIONS FOR STIMULATING AXON REGENERATION AND PREVENTING NEURONAL CELL DEGENERATION

<130> ERM-105.01

<160> 4

<170> PatentIn version 3.0

<210> 1

<211> 1050

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (32)..(751)

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ggg tac gat aac cgg gag ata gtg atg aag tac atc cat tat aag ctg	100	
Gly Tyr Asp Asn Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu		
10	15	20

tcg cag agg ggc tac gag tgg gat gcg gga gat gtg ggc gcc gcg ccc	148	
Ser Gln Arg Gly Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro		
25	30	35

ccg ggg gcc ccc gcg ccg ggc atc ttc tcc tcg cag ccc ggg cac	196		
Pro Gly Ala Ala Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His			
40	45	50	55

acg ccc cat aca gca tcc cgg gac ccg gtc gcc agg acc tcg ccg	244	
Thr Pro His Thr Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro		
60	65	70

ctg cag acc ccg gct gcc ccc ggc gcc gcc gcg ggg cct gtc agc	292	
Leu Gln Thr Pro Ala Ala Pro Gly Ala Ala Gly Pro Ala Leu Ser		
75	80	85

ccg gtg cca cct gtg gtc cac ctg acc ctc cgc cag gcc ggc gac gac	340	
Pro Val Pro Pro Val Val His Leu Thr Leu Arg Gln Ala Gly Asp Asp		
90	95	100

ttc tcc cgc cgc tac cgc cgc gac ttc gcc gag atg tcc agg cag ctg	388	
Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met Ser Arg Gln Leu		
105	110	115

cac ctg acg ccc ttc acc gcg cgg gga cgc ttt gcc acg gtg gtg gag	436		
His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu			
120	125	130	135

gag ctc ttc agg gac ggg gtg aac tgg ggg agg att gtg gcc ttc ttt	484
Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe	

20491311.1

	140	145	150		
gag ttc ggt ggg gtc atg tgt gtg gag agc gtc aac cg ^g gag atg tcg Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser	155	160	165	532	
ccc ctg gtg gac aac atc gcc ctg tgg atg act gag tac ctg aac cg ^g Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg	170	175	180	580	
cac ctg cac acc tgg atc cag gat aac gga ggc tgg gat gcc ttt gtg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val	185	190	195	628	
gaa ctg tac ggc ccc agc atg cg ^g cct ctg ttt gat ttc tcc tgg ctg Glu Leu Tyr Gly Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu	200	205	210	215	676
tct ctg aag act ctg ctc agt ttg gcc ctg gtg gga gct tgc atc acc Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr	220	225	230	724	
ctg ggt gcc tat ctg ggc cac aag tga agtcaacatg cctggcccaa Leu Gly Ala Tyr Leu Gly His Lys	235			771	
acaaatatgc aaaaggttca ctaaagcagt agaaataata tgcattgtca gtgatgttcc				831	
atgaaacaaa gctgcaggct gtttaagaaa aaataacaca catataaaca tcacacacac				891	
agacagacac acacacacac aacaattaac agtcttcagg caaaacgtcg aatcagctat				951	
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Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met	1	5	10	15
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala	20	25	30	
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile	35	40	45	
Phe Ser Ser Gln Pro Gly His Thr Pro His Thr Ala Ala Ser Arg Asp	50	55	60	
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala				

65

70

75

80

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr
 85 90 95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe
 100 105 110

Ala Glu Met Ser Arg Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
 115 120 125

Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
 130 135 140

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
 145 150 155 160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190

Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
 195 200 205

Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
 210 215 220

Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Gly His Lys
 225 230 235

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<212> DNA

<213> homo sapiens

<220>

<221> CDS

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aaccagagac gagactcagt gagtgagcag gtgtttgga caatggactg gttgagccca 120

tccctattat aaaa atg tct cag agc aac cgg gag ctg gtg gtt gac ttt 170
 Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe
 1 5 10

ctc tcc tac aag ctt tcc cag aaa gga tac agc tgg agt cag ttt agt 218
 Leu Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser
 15 20 25

gat gtg gaa gag aac agg act gag gcc cca gaa ggg act gaa tcg gag 266
 Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu
 30 35 40

atg gag acc ccc agt gcc atc aat ggc aac cca tcc tgg cac ctg gca Met Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala 45 50 55 60	314
gac agc ccc gcg gtg aat gga gcc act gcg cac agc agc agt ttg gat Asp Ser Pro Ala Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp 65 70 75	362
gcc cg ^g gag gtg atc ccc atg gca gca gta aag caa g ^g ctg agg gag Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu 80 85 90	410
gca ggc gac gag ttt gaa ctg cg ^g tac cg ^g gca ttc agt gac ctg Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu 95 100 105	458
aca tcc cag ctc cac atc acc cca ggg aca gca tat cag agc ttt gaa Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu 110 115 120	506
cag gta gtg aat gaa ctc ttc cg ^g gat ggg gta aac tgg ggt cg ^c att Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile 125 130 135 140	554
gtg gcc ttt ttc tcc ttc ggc ggg gca ctg tgc gtg gaa agc gta gac Val Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp 145 150 155	602
aag gag atg cag gta ttg gtg agt cg ^g atc gca gct tgg atg gcc act Lys Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr 160 165 170	650
tac ctg aat gac cac cta gag cct tgg atc cag gag aac ggc ggc tgg Tyr Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp 175 180 185	698
gat act ttt gtg gaa ctc tat ggg aac aat gca gca gcc gag agc cga Asp Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Glu Ser Arg 190 195 200	746
aag ggc cag gaa cg ^c ttc aac cg ^c tgg ttc ctg acg ggc atg act gtg Lys Gly Gln Glu Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val 205 210 215 220	794
gcc ggc gtg gtt ctg ctg ggc tca ctc ttc agt cg ^g aaa tga Ala Gly Val Val Leu Leu Gly Ser Leu Phe Ser Arg Lys 225 230	836
ccagacactg accatccact ctaccctccc acccccttct ctgctccacc acatcctccg	896
tccagccgccc attgccacca ggagaacccg	926

<210> 4
<211> 233
<212> PRT

<213> homo sapiens

<400> 4

Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe Leu Ser Tyr Lys
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Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser Asp Val Glu Glu
20 25 30

Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu Met Glu Thr Pro
35 40 45

Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala Asp Ser Pro Ala
50 55 60

Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp Ala Arg Glu Val
65 70 75 80

Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu Ala Gly Asp Glu
85 90 95

Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu Thr Ser Gln Leu
100 105 110

His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu Gln Val Val Asn
115 120 125

Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe
130 135 140

Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp Lys Glu Met Gln
145 150 155 160

Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr Tyr Leu Asn Asp
165 170 175

His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp Asp Thr Phe Val
180 185 190

Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg Lys Gly Gln Glu
195 200 205

Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val Ala Gly Val Val
210 215 220

Leu Leu Gly Ser Leu Phe Ser Arg Lys
225 230